

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on:

March 13, 2003, 23:55:25 ; Search time 6291 Seconds

(without alignments)

9918.362 Million Cell updates/sec

Title: US-09-698-781-2

Perfect score: 2144

Sequence: 1 tgatdaaacaataacttcat.....aaaaaaaaaaaaaaaa 2144

Scoring table: IDENTITY_NUC

gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database :

GenEmpl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_v1:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_lov:*

23: em_pat:*

24: em_lp1:*

25: em_ro:*

26: em_lp1:*

27: em_sts:*

28: em_v1:*

29: em_htg_hum:*

30: em_htg_inv:*

31: em_htg_other:*

32: em_htg_mus:*

33: em_htg_pln:*

34: em_htg_rid:*

35: em_htg_rnt:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

SUMMARES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2144	100.0	2144	6	AX127587	AX127587 Sequence
2	2134.8	99.6	2138	9	HSSP038	X94323 Homo sapiens m
3	2113.2	98.6	2128	6	AX335634	AX335634 Sequence
4	2113.2	98.6	2128	9	HSCR1SP3G	X93240 Homo sapiens m
5	1485.2	69.3	151752	2	AC010779	AC010779 Homo DNA
6	1480.4	69.0	118524	9	HSDD412L6	AL121950 Human DNA
7	515.2	24.0	1335	9	HUMTP1A	M2532 Human testis
8	513.6	24.0	1380	9	BC022011	X92239 Homo sapi
9	513.6	24.0	1406	9	HSCR1SP2I	X92239 Homo sapiens m
10	505.8	23.6	1295	4	ECCR1SP3	AJ001400 Equus cab
11	476.2	22.2	1388	10	CPR35712	U55712 Cavia porce
12	370.8	17.3	1418	10	MUSTX1A	M25533 Mouse testis
13	367.8	17.2	1280	10	AB009662	AB009662 Rattus no
14	362.2	16.9	1432	10	AF078552	AF078552 Rattus no
15	362.2	16.9	1498	10	RATAG	M31173 Rat epididy
16	346.4	16.2	1380	10	MUSAG1A	M02849 Mouse acid
17	346.4	16.2	1403	10	MUSCR1SPA	L05559 Mouse cyste
18	341.6	15.9	1445	10	BC011150	BC011150 Mus mus
19	325.6	15.2	928	10	RNESCR	X06433 Rat mRNA fo
20	325.4	15.2	495	4	ECA662	AJ006632 Equus cab
21	294.4	13.7	453	4	BTA277708	AJ277708 Bos tauru
22	287.6	13.4	1394	10	MUSAG2A	M02850 Mouse acid
23	287.6	13.4	1418	10	BC022573	BC022573 Mus mus
24	287	13.4	1406	10	MUSC1LSPB	L03560 Mouse cyste
25	254.4	11.9	256	6	AX127586	AX127586 Sequence
26	226.4	10.6	1090	10	U13619	U13619 Heloderma h
27	210.8	9.8	334	4	BTA277709	AJ277709 Bos tauru
28	205	9.6	1336	5	AF384218	AF384218 Agkistrodon
29	202.4	9.4	1321	5	AF384219	AF384219 Trimeresurus
30	198.6	9.3	791	5	AY093955	AY093955 Rhabdophis
31	198.6	9.3	1318	5	PMU59447	U59447 Trimeresurus
32	183	8.5	51371	9	AL353193	AL353193 Human DNA
33	182.8	8.5	169189	2	AC124008	AC124008 Equus cab
34	182.4	8.5	1309	5	AF190561	AF190561 Equus cab
35	182	8.5	1475	4	ECA315379	AJ315379 Equus cab
36	180.8	8.4	1305	2	AF384220	AF384220 Equus cab
37	179.8	8.4	15869	2	AC023420	AC023420 Homo sapi
38	177.4	8.3	1316	5	AF159541	AF159541 Lepomis h
39	177	8.3	1281	9	D38451	D38451 Homo sapi
40	177	8.3	1282	9	S80310	S80310 acidic epid
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42	175.6	8.2	1174	4	ECA6631	AJ006631 Equus cab
43	173.4	8.1	149907	4	AC091436	AC091436 Felis cat
44	170.2	7.9	16287	9	AC026643	AC026643 Homo sapi
45	169.2	7.9	1343	9	AF123894	AF123894 Macaca mu

ALIGNMENTS

RESULT	1	AX127587	AX127587	Sequence 2	from Patent WO0131343.	DNA	linear	PAT 15-MAY-2001
DEFINITION								
ACCESSION								
VERSION								
KEYWORDS								
SOURCE								
ORGANISM								
Homo sapiens								
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;								
1 (bases 1 to 2144)								
Hubert,R.S., Raitano,A.B., Afar,D.E., Mitchell,S.C., Farts,M. and								
Jakobovits,A.								
REFERENCE								
AUTHORS								
TITLE								
Diagnosis and therapy of cancer using sgp28-related molecules								

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0131343-A 2 03-MAY-2001;
 Urogenesis, Inc. (US) Location/Qualifiers
 FEATURES source
 BASE COUNT 735 a /db_xref="taxon:9606"
 ORIGIN 403 c 382 g 624 t

Query Match 100 %; Score 2144; DB 6; Length 2144;
 Best Local Similarity 100 %; Pred. No. 0;
 Matches 2144; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

QY 1 TGATGAAACAATACTTCATCCTGCTCTGGAAACACTGCATAGACATATTCCAGTG 60
 Db 1 TGATGAAACAATACTTCATCCTGCTCTGGAAACACTGCATAGACATATTCCAGTG 60

QY 61 TGTGCTCCCTGGTGTGGCTGGCTGCCTCCATCTTCCAGCAATGAGATAGGATCCG 120
 Db 61 TGTGCTCCCTGGTGTGGCTGCCTCCATCTTCCAGCAATGAGATAGGATCCG 120

QY 121 CTTTACTGCCTTGTAACCAACCAACACAGACAGTCACAAGGGAGTTGGAAATAGCACA 180
 Db 121 CTTTACTGCCTTGTAACCAACCAACACAGACAGTCACAAGGGAGTTGGAAATAGCACA 180

QY 181 ATGAACTGAGGAGGAGCAGTATCCTCCCTGCCAGAACATCTGAGAAGGAGATGGAA 240
 Db 181 ATGAACTGAGGAGGAGCAGTATCCTCCCTGCCAGAACATCTGAGAAGGAGATGGAA 240

QY 241 AAGGGCTGCAGCAATGCCAACAGTGGCAACAGCAGTCATAGACACAACTAAC 300
 Db 241 AAGGGCTGCAGCAATGCCAACAGCAGTCATAGACACAACTAAC 300

QY 301 CAAGGATCCAAATGACAAGCTCTAAATATGTTGAGAATCTACATGTCAGTGCCCCA 360
 Db 301 CAAGGATCCAAATGACAAGCTCTAAATATGTTGAGAATCTACATGTCAGTGCCCCA 360

QY 361 GCTCAGGTCACAACTCAAACTGCTTAAATGTTGAGTCATGTCAGTGCCCCA 360
 Db 361 GCTCAGGTCACAACTCAAACTGCTTAAATGTTGAGTCATGTCAGTGCCCCA 360

QY 421 TAGGCCAAGAGCTCCAAAGCAGTGGTGGACATATACACAGCTGTTGGFACTCT 480
 Db 421 TAGGCCAAGAGCTCCAAAGCAGTGGTGGACATATACACAGCTGTTGGFACTCT 480

QY 481 CATACTCGTGTGAACTGCTTAAATGTTGAGTCATGTCAGTGAGTATGTTGTTG 420
 Db 481 CATACTCGTGTGAACTGCTTAAATGTTGAGTCATGTCAGTGAGTATGTTGTTG 420

QY 541 ATGTTGCCATATGTCCTGCTGTAATGGCTAAATGACTATATGTCCTTATGAA 600
 Db 541 ATGTTGCCATATGTCCTGCTGCTGTAATGGCTAAATGACTATATGTCCTTATGAA 600

QY 601 AAGGGACACCTGGCCAGTGTGACATGACTGACATGACTATGACCTGGT 660
 Db 601 AAGGGACACCTGGCCAGTGTGACATGACTGACATGACTATGACCTGGT 660

QY 661 GCAAGTACCAAGACTCTATAGTACTGAACTTGTGAACTGACATTAACCTGAAC 720
 Db 661 GCAAGTACCAAGACTCTATAGTACTGAACTTGTGAACTGACATTAACCTGAAC 720

QY 721 ATCAGTGGTCAGGAGCAGTGTGAACTGACATGACTATGACCTGGT 780
 Db 721 ATCAGTGGTCAGGAGCAGTGTGAACTGACATGACTATGACCTGGT 780

QY 781 TACGGATTACACCGAGTAGGCTATGTAGAGGAGTCAGTATCTACTAGATTG 840
 Db 781 TACGGATTACACCGAGTAGGCTATGTAGAGGAGTCAGTATCTACTAGATTG 840

QY 841 GCATCTACTATAGTAACTACTAGTGTGAAATCTGACATGTCAGTGTGACACATT 900
 Db 841 GCATCTACTATAGTAACTACTAGTGTGAAATCTGACATGTCAGTGTGACACATT 900

QY 901 TGATTCAAATGTTCTCTGGATCTGCCTTATTACAAATATTTCATACA 960
 Db 901 TGATTCAAATGTTCTCTGGATCTGCCTTATTACAAATATTTCATACA 960

QY 961 ATGGTTAAAGAGAACAACTCTAAACACAACTTGGATTATATAACTTG 1020
 Db 961 ATGGTTAAAGAGAACAACTCTAAACACAACTTGGATTATATAACTTG 1020

QY 1021 TGATTAATTACTGAATTAATTAGGGAAATTGAAACTGTATTCATAGA 1080
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QY 1081 CTAAGTCTAAACCCGATGAAATTAGGTCAGAAATTGTCAGAACATGTAGA 1140
 Db 1081 CTAAGTCTAAACCCGATGAAATTAGGTCAGAAATTGTCAGAACATGTAGA 1140

QY 1141 AAAGACAAATAATTACATGACCCCTGGCTGATSTGCTTCTAGTCACCT 1200
 Db 1141 AAAGACAAATAATTACATGACCCCTGGCTGATSTGCTTCTAGTCACCT 1200

QY 1201 CTAAGCTAAAGCATCTCAAGACGCTTCCCATATGCTGCTTAATTTCACCT 1260
 Db 1201 CTAAGCTAAAGCATCTCAAGACGCTTCCCATATGCTGCTTAATTTCACCT 1260

QY 1261 TCACCTTCTCCAACTCTGGCTGGCATCTCACATGTCAGTGAACCTGTC 1320
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QY 1321 TAAACATCTGACTTTTGGCAAACTACATACATCCTTGAATTTCATCTG 1380
 Db 1321 TAAACATCTGACTTTTGGCAAACTACATACATCCTTGAATTTCATCTG 1380

QY 1381 CATAATTTCAGTAAAGATATGATCAACCTCTCATTTAACCTCTTGTG 1440
 Db 1381 CATAATTTCAGTAAAGATATGATCAACCTCTCATTTAACCTCTTGTG 1440

QY 1441 AAACTCTCTAAAGATAACAGATAATAGTAAATACCTCCACTCAGGGAC 1500
 Db 1441 AAACTCTCTAAAGATAACAGATAATAGTAAATACCTCCACTCAGGGAC 1500

QY 1501 AGAACTCAGTCCTCCCTTGACTCTACTAAATCAGTACTCTCCAAAGCT 1560
 Db 1501 AGAACTCAGTCCTCCCTTGACTCTACTAAATCAGTACTCTCCAAAGCT 1560

QY 1561 GGAGTGTGAAAGGAACATAGTAACTTACAGGGGAAATGACAAATGAGCT 1620
 Db 1561 GGAGTGTGAAAGGAACATAGTAACTTACAGGGGAAATGACAAATGAGCT 1620

QY 1621 CACCAAGTGTGAACTTACAGTCACAGTAACTGTCAGTATGTCAGTAACTG 1680
 Db 1621 CACCAAGTGTGAACTTACAGTCACAGTAACTGTCAGTATGTCAGTAACTG 1680

QY 1681 CTTCCTAAATCTACAACTCTCTTGTGAACTTCAGCTTCAACCTCAACTG 1740
 Db 1681 CTTCCTAAATCTACAACTCTCTTGTGAACTTCAGCTTCAACCTCAACTG 1740

QY 1741 TGAGGACTCTCAAAATCTCCCTGGTATTGTGAACTCTAACACTGAA 1800
 Db 1741 TGAGGACTCTCAAAATCTCCCTGGTATTGTGAACTCTAACACTGAA 1800

QY 1801 ATCATGAAATAAGGGAACTCTGAGAACATCACAGCACAGTGAAGGAGCA 1860
 Db 1801 ATCATGAAATAAGGGAACTCTGAGAACATCACAGCACAGTGAAGGAGCA 1860

QY 1861 TGTGACCAATGCAATGCTCTTGGTCAATTCGGACAGAACAGTCAAT 1920
 Db 1861 TGTGACCAATGCAATGCTCTTGGTCAATTCGGACAGAACAGTCAAT 1920

QY 1921 GAAAACATGAGTCAGTGAATGAACTGGGATTTAACAGTACTGTGATTG 1980
 Db 1921 GAAAACATGAGTCAGTGAATGAACTGGGATTTAACAGTACTGTGATTG 1980

QY 1981 TAATCTGACAATATAGGGAAATGTAAGATGATAACGTAGAGAACCTGG 2040

Db	61	CCATCTTCCCGAAATGAAGATAAGGATCCCGCTTACTGCTTGTAAACCCAA	120	Qy	147	ACACAAGTGCAGAACAGGGAGATGTGAATAAGCACATGAACTGGAGGAGCAGTCTCC	206	Db	121	ACACAGTGCAGAACAGGGAGATGTGAATAAGCACATGAACTGGAGGAGCAGTCTCC	180	Qy	207	CTGGCAGAACATCGTGAAGATGGAAAGGACAAAGAGGCTGCAGCAATGCCAAAG	266	Db	181	CTGGCAGAACATCGTGAAGATGGAAAGGAGGCTGCAGCAATGCCAAAG	240	Qy	267	TGGCAACACAGTGCATTAGACAGACAGAACAGATGCAAGTAAAGGATCGAAGCTAAA	326	Db	241	TGGCAACACAGTGCATTAGACAGACAGAACAGATGCAAGTAAAGGATCGAAGCTAAA	300	Qy	327	TCTGGAGAACATCTCATACATGCAACTGCCAGTGCCAGTGTCAAGCAAGCTAAC	386	Db	301	TCTGGAGAACATCTCATACATGCAACTGCCAGTGCCAGTGTCAAGCAAGCTAAC	360	Qy	387	TGGTTGATGAGTACATGATTGACTTGGTNGGCCAAAGACTCCACCGAGT	446	Db	361	TGGTTGATGAGTACATGATTGACTTGGTNGGCCAAAGACTCCACCGAGT	420	Qy	447	GTGGACATATACAGAGGTGTTGACTCTCATACCTGGTGGATGGAAATGCC	506	Db	421	GTGGACATATACAGGTGTTGACTCTCATACCTGGTGGATGGAAATGCC	480	Qy	507	TACTGTCACAAAGTCTAAATAACTACTATGTTGCAATTGCTGCTGGT	566	Db	481	TACTGTCACAAAGTCTAAATAACTACTATGTTGCAATTGCTGCTGGT	540	Qy	567	ATTSGGCTAACTAGCTATGTCCTATGACAAAGGACCCGTGGAGTGGCCA	626	Db	541	ATTSGGCTAACTAGCTATGTCCTATGACAAAGGACCCGTGGAGTGGCCA	600	Qy	627	GATACTGTGAGATGACTATGTCCTATGACAAAGGACCCGTGGAGTGGCA	686	Db	601	GATACTGTGAGATGACTATGTCCTATGACAAAGGACCCGTGGAGTGGCA	660	Qy	687	TGAAAGTTGAGTCACITTAACCTGAAACATCAGTGTAGGAGATGCAAG	746	Db	661	TGAAAGTTGAGTCACITTAACCTGAAACATCAGTGTAGGAGATGCAAG	720	Qy	747	GCTCTGCAATGTCACACAGCATTTAACCGGAGTAGGCTA	806	Db	721	GCTCTGCAATGTCACACAGCATTTAACCGGAGTAGGCTA	780	Qy	807	TGTAAGGAGGTGAGTACATGACTAGTTGCACTTGATTAACATGAGCT	866	Db	781	TGTAAGGAGGTGAGTACATGACTAGTTGCACTTGATTAACATGAGCT	840	Qy	867	AGCTGAAATTGAGTCACATGACTAGTTGCACTTGATTAACATGAGCT	926	Db	841	AGCTGAAATTGAGTCACATGACTAGTTGCACTTGATTAACATGAGCT	900	Qy	927	CTGCTTTTATTTACAAATTTCTACAAATGGTAAAGAACAAATCTAT	986	Db	901	CTGCTTTTATTTACAAATTTCTACAAATGGTAAAGAACAAATCTAT	960	Qy	987	ACACAGACTTGGATTATAAACCTTGATTAATCTGATTAATCTGATTA	1046	Db	961	ACACAGACTTGGATTATAAACCTTGATTAATCTGATTAATCTGATTA	1020	Qy	1047	GGGTGAATAATTGAAAGTGTATCTCATATGACTAACCTGGATTA	1106	Db	1021	GGGTGAATAATTGAAAGTGTATCTCATATGACTAACCTGGATTA	1080	Qy	1107	AGTGAATAATTGTCAGACAAATGTCACAAAGAACATAATTCTACATGA	1166	Db	1081	AGTGAATAATTGTCAGACAAATGTCACAAAGAACATAATTCTACATGA	1140	Qy	1167	ACCTGGCTAGTGCCTTCTAGACAAATGTCACAAAGAACATAATTCTACATGA	1226	Db	1141	ACCTGGCTAGTGCCTTCTAGCTCCACTCTAGCTAACAGCTTCAGAGCT	1200
RESULT	5			Qy	1227	TTCCTCATATGCTGCTTAATCTCTTCACTTCACCTCCTCTCCCAATCATCTGGCT	1286	Db	1201	TTCCTCATATGCTGCTTAATCTCTTCACTTCACCTCCTCTCCCAATCATCTGGCT	1260	Qy	1287	GGCATCTCACATTGAGTGTGCTCTCTCAACATCCGACTTTATTTGC	1346	Db	1261	GGCATCTCACATTGAGTGTGCTCTCTCAACATCCGACTTTATTTGC	1320	Qy	1347	CAAACTACATCCTGATTTTACGTGATAATTAGCTAGATGATGCT	1406	Db	1321	CAAACTACATCCTGATTTTACGTGATAATTAGCTAGATGATGCT	1380	Qy	1407	AAACCTCTTTAACCTCTCTCTCAACATCCGACTTTAAGAATACAAG	1466	Db	1381	AAACCTCTTTAACCTCTCTCTCAACATCCGACTTTAAGAATACAAG	1440	Qy	1467	ATAATAGCTAACTACCTCCACTCAGGGAGTAACTCAGTCTGAGATGTC	1526	Db	1441	ATAATAGCTAACTACCTCCACTCAGGGAGTAACTCAGTCTGAGATGTC	1500	Qy	1507	CTCACATTAATCTGCAATTGCTCAAGTGTCAATTGCTCAAACTCTAAC	1586	Db	1501	CTTCACATTAATCTGCAATTGCTCAAGTGTCAATTGCTCAAACTCTAAC	1560	Qy	1587	CTTACAGGGAGAAATGACAATGAGCTGCTTCAACAGTGTCAATTGCTCAAC	1646	Db	1561	CTTACAGGGAGAAATGACAATGAGCTGCTTCAACAGTGTCAATTGCTCAAC	1620	Qy	1647	CAGTAACTGCTTCACTGACTCTGCTTCAACAGTGTCAATTGCTCAAC	1706	Db	1621	CAGTAACTGCTTCACTGACTCTGCTTCAACAGTGTCAATTGCTCAAC	1680	Qy	1707	TAATTGAGCTAACATCCAGAAACTCACTCCAGTGTAGGAGTGGAA	1766	Db	1681	TAATTGAGCTAACATCCAGTGTAGGAGTGGAA	1740	Qy	1767	GGGTATTAGTAGTTCTCAAACTGTAATCTGAAATGGAGTCTGAG	1826	Db	1741	GGGTATTAGTAGTTCTCAAACTGTAATCTGAAATGGAGTCTGAG	1800	Qy	1827	AAACATCAGACCACTGAGACTAGGAGACATGTGAGCAATGTCCT	1886	Db	1801	AAACATCAGACCACTGAGACTAGGAGACATGTGAGCAATGTCCT	1860	Qy	1887	GGTCACTGAGTACATGAGCTTCAACACTGAGTAACTCTGAGAATGGAGTCTGAG	1946	Db	1861	GGTCACTGAGTACATGAGCTTCAACACTGAGTAACTCTGAGAATGGAGTCTGAG	1920	Qy	1947	ATCTGGAGTATTCTACAGTGTGCTTCACTGAGCTTCAACATGTCCT	2006	Db	1921	ATCTGGAGTATTCTACAGTGTGCTTCACTGAGCTTCAACATGTCCT	1980	Qy	2007	TGTAAGTGTAACTGAGTGTGAGACTGAGCTGAGACATGTGAGCAATGTCCT	2066	Db	1981	TGTAAGTGTAACTGAGTGTGAGACTGAGCTGAGACATGTGAGCAATGTCCT	2040	Qy	2067	ACTATCTACCAATTTCGGTAGCTGCTAGCAACGAAATTAAGAGTCTGA	2126	Db	2041	ACTATCTACCAATTTCGGTAGCTGCTAGCAACGAAATTAAGAGTCTGA	2100	Qy	2127	AAAAAAAGAAAAAAAGAAAAAAAGAAAAAAAGAAAAAAAGAAAAAA	2144	Db	2101	AAAAAAAGAAAAAAAGAAAAAAAGAAAAAAAGAAAAAAAGAAAAAA	2118																

AC010779/C
DEFINITION Homo sapiens clone RP1-3A4, WORKING DRAFT SEQUENCE, 11 unordred pieces.
ACCESSION AC010779
VERSION AC010779.4 GI:9369464

KEYWORDS HTGS_PHASE1; HTGS_DRAFT.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

REFERENCE 1 (bases 1 to 151752)
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 151752)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckley, R., Boguslavsky, L., Boukhalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeAngelis, K., Devar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardya, S., Grant, G., Hafos, B., Heaford, A., Hilton, J., Howland, J. C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lenoczyk, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McCurk, A., McKernan, K., McLaughlin, J., Melodim, J., Morrow, J., Naylor, J., Norman, O., O'Conor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, J., Severy, P., Strange-Thomann, N., Stolanoian, A., Talamas, J., Vassiliev, H., Vo, A., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.

TITLE Direct Submission

JOURNAL Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT Submitted (22-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jul 22, 2000 this sequence version replaced g1:7321560.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information

Center project name: L299
 Center clone name: 3_A_4

----- Summary Statistics

Sequencing vector: M13; M7815; 100% of reads
 Chemistry: Dye-Terminator Big Dye; 100% of reads
 Assembly program: PIRAP; version 0.960731
 Consensus quality: 142917 bases at least 040
 Consensus quality: 14690 bases at least 030
 Consensus quality: 148664 bases at least 020
 Insert size: 150000; agarose-fp
 Insert size: 150752; sum-of-contigs
 Quality coverage: 4.8 in Q20 bases; agarose-fp
 Quality coverage: 4.8 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1901: contig of 1901 bp in length
 * 1902 2001: gap of 100 bp
 * 2002 4631: contig of 2630 bp in length
 * 4632 4731: gap of 100 bp
 * 4732 9747: contig of 5015 bp in length
 * 9846: gap of 100 bp
 * 9847 17668: contig of 7823 bp in length
 * 17670 17769: gap of 100 bp
 * 17770 29964: contig of 12195 bp in length
 * 29965 30064: gap of 100 bp
 * 30065 43491: contig of 12433 bp in length
 * 43598 43597: gap of 100 bp
 * 43598 60340: contig of 16743 bp in length
 * 60341 60440: gap of 100 bp

BASE COUNT 49163 a 27268 c 27224 g 47065 t 1032 others
 ORIGIN

Query Match	Score	DB	Length
Best Local Similarity	69.3%	2	151752
Matches	1487	Conservative	0
Best Local Similarity	54.8%	Pred. No.	5e-264
Matches	3	Mismatches	3
Indels	0	Gaps	0

QY 652 CCAATGTTGCAAGTACGAGATCTCTATACTAATCTGAAAGTTGAGCTCACCAA 711
 DB 80106 CCAATGGTTGCAAGTACGAGATCTCTATACTGAAAGTTGAGCTCACCAA 80047

QY 712 CCTGTAACATCAGTGGCAGGAGCTGCAAGGCATCTGCAATTGTCAACAGCA 771
 DB 80046 CCTGTAACATCAGTGGCAGGAGCTGCAAGGCATCTGCAATTGTCAACAGCA 79987

QY 772 TTATTAATAGCATACACCCGACTAGGGCTATAGAGGGTAGAGCTATCTAC 831
 DB 79986 TTATTAATAGCATACACCCGACTAGGGCTATAGAGGGTAGAGCTATCTAC 79927

QY 832 TTAGATTTGGCATCTACTAGTAACTATACTAGCTGAGAATTGAGCTATGTG 891
 DB 79926 TTAGATTTGGCATCTACTAGTAACTATACTGAGAATTGAGCTATGTG 79867

QY 892 ATACACITGTTGATCAAGTGTCTCTGAGCTGCTTTATTACAAATATT 951
 DB 79866 ATACACATGTTGATCAAGTGTCTCTGAGCTGCTTTATTACAAATATT 79807

QY 952 TTTCATACAAATGGTAAAGAACAACTATACAAACACTTGTGAGTTATA 1011
 DB 79806 TTTCATACAAATGGTAAAGAACAACTATACAAACACTTGTGAGTTATA 79747

QY 1012 TAACTTGTGATTAATTAATCTGAATTAATAGGGAAATTGAAAGTGTAT 1071
 DB 79746 TAACTTGTGATTAATTAATCTGAATTAATAGGGAAATTGAAAGTGTAT 79687

QY	832	TTAGATTGCACTACTAGATTAACTACATACTAGCTGAGAATGAGGCACTG	891
Db	117559	TTAGATTGCACTACTAGATTAACTACATACTAGCTGAGAATGAGGCACTG	117500
QY	892	ATACACATTGATTCAATAGTTCTCTGATCTGCTGTTTATTACAAATAT	951
Db	117499	ATACACATTGATTCAATAGTTCTCTGATCTGCTGTTTATTACAAATAT	117440
QY	952	TTTCATACAAAGGTAAAGAACAAATCTATACACAACTTGGATTATA	1011
Db	117439	TTTCATACAAAGGTAAAGAACAAATCTATACACAACTTGGATTATA	117380
QY	1072	CTCATAGACTAGTCACTAAACCTGTGATGAAAGTAAATTGTTCTAGAAC	1131
Db	117319	CTCATAGACTAGTCACTAAACCTGTGATGAAAGTAAATTGTTCTAGAAC	117260
QY	1132	AAATCTACAAAGAACAAATATTTCACATGAACTGACCCCTGGCTAGTGCTT	1191
Db	117259	AAATCTACAAAGAACAAATATTTCACATGAACTGACCCCTGGCTAGTGCTT	117200
QY	1192	ACCTCCACTCTAGGCTAAAGCATCTGAAAGGTTCCCATATGCTGCTTATTCT	1251
Db	117199	ACCTCCACTCTAGGCTAAAGCATCTGAAAGGTTCCCATATGCTGCTTATTCT	117140
QY	1252	TTACACTATCACCCTCTCCCATATCATCTGCTGCTGGCATCCACAAATTGAGC	1311
Db	117139	TTACACTATCACCCTCTCCCATATCATCTGCTGCTGGCATCCACAAATTGAGC	117080
QY	1312	TGTTCTCCCTAAACAACTCTGACTTTATTTGCCAAATCATACATCCCTTGAA	1371
Db	117079	TGTTCTCCCTAAACAACTCTGACTTTATTTGCCAAATCATACATCCCTTGAA	117020
QY	1372	TTTACTCTGATAATTACAGTAGATGATGATAAACCTCTGTTAACCTCTCT	1431
Db	117019	TTTACTCTGATAATTACAGTAGATGATGATAAACCTCTGTTAACCTCTCT	116960
QY	1432	CTCTTGACAAACTCCTTAAAGAACTACAGATAATACCTCCACT	1491
Db	116959	CTCTTGACAAACTCCTTAAAGAACTACAGATAATACCTCCACT	116900
QY	1492	CAAGGAGTGTGACTCTGCTCTCCCTGAGCTCTCAAAATCAGTCAACT	1551
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QY	1552	CCAAGAGTGGAGTATGAAAGGAACTAGTACAGGGAGAAATGACAA	1611
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QY	1612	TGACGCTTCAACAACTGATGAAATTAAGGCAACCGTGTAAAGTCATCGATGTT	1671
Db	116779	TGACGCTTCAACAACTGATGAAATTAAGGCAACCGTGTAAAGTCATCGATGTT	116720
QY	1672	CTAGATACTCTAAATCATACCCATCTATATGAGCTAAAGATCCAGCA	1731
Db	116719	CTAGATACTCTAAATCATACCCATCTATATGAGCTAAAGATCCAGCA	11660
sig-peptide			
QY	1732	ACTCTAGTGTAGGACATCTACAAATATCCCTGGTATTAGTTCCTCAA	1791
Db	116659	ACTCTAGTGTAGGACATCTACAAATATCCCTGGTATTAGTTCCTCAA	11660
QY	1792	ACTGTTAAACATGAAATGAAATGAGGAACTTACAGACAACTACAGACATGAGCT	1851
Db	116599	ACTGTTAAACATGAAATGAAATGAGGAACTTACAGACAACTACAGACATGAGCT	116540
QY	1852	AGGGAGACAGTGGCAAATGCAATGTCCTCTGGATCAGATCTGGACAGAAAG	1911
Db	116539	AGGGAGACAGTGGCAAATGCAATGTCCTCTGGATCAGATCTGGACAGAAAG	116480
Query Match 24.0%; Score 515.2; DB 9; Length 1335; Best Local Similarity 68.8%; Pred. No. 4; e-5; Matches 798; Conservative 0; Mismatches 323; Indels 39; Caps 5; Origin Chromosome 6.			
RESULT 7			
HUMTPX1A HUMTPX1A			
DEFINITION Human testis-specific protein (TPX-1) mRNA, complete cds.			
ACCESSION M2532.J04741			
VERSION M2532.1			
KEYWORDS testis-specific protein.			
SOURCE Human adult testis, cDNA to mRNA, clones H4-1 and p3-1.			
ORGANISM Homo sapiens			
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
REFERENCE 1 (bases to 1335)			
AUTHORS Kasahara, M., Gutknecht, J., Brew, K., Spur, N. and Goodfellow, P.N.			
TITLE Cloning and mapping of a testis-specific gene with sequence similarity to a sperm-coating glycoprotein gene			
JOURNAL Genomics 5 (3), 527-534 (1989)			
MEDLINE 9029048			
PUBMED 2613236			
COMMENT Draft entry and computer-readable sequence for [1] kindly submitted by M. Kasahara, 09-JUN-1989.			
FEATURES source			
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190. .249			
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428 a 279 c 271 g 355 t 2 others			
BASE COUNT			
ORIGIN			

Db	142 TATAAAGTAGTATTCATCCTGCTCAGAAACATTTCCACCAATGGTACATTCTGAAACAT	Db	1188 TAGGATTAGGTTCACTAGACTTGGATCAAATGGTCATTACGTATTCTGAAACAT
Oy	57 GTGCTGTGTTCTGGTCGGGCTCTCCATTTCCAGCAATGAGATAGGAT 116	Oy	1136 GTCACAAAGAACAAATATAA 1155
Db	202 CGGCTGTGTTCTGGTACTCTGCGTCCTCCATCTTACGTCA--GAAGGAAGGT 258	Db	1248 GCTAACAGAGAGACTGTTAA 1267
Oy	117 CCCGCTTTACTGCTTGTAAACCACCCAACAAACAGTCAGAGGAGATGTGATAAG 176		RESULT 8
Db	259 CCCGCTTTACTGCTTGTAAACCACCGTGCAGNTGCAAGGAGATGTGATAAA 318	BC022011	BC02011 1380 bp mRNA linear PRI 24-JAN-2002
Oy	177 CAAATGAACTGGAGGAGCAGTATCTCCCTGGCAAAGAACATGTAAGATGGATGG 236	DEFINITION	Homo sapiens, testis specific protein 1 (probe H4-1 p3-1), clone MGC:26358 IMAGE:4826427, mRNA, complete cds.
Db	319 CAAATGAACTGGAGGAGCAGTCTCCACCTGGCAAGTAAAGCTTAAGTGGATGG 378	ACCESSION	BC02011
Oy	237 AACAAAGAGGTGGCAAACTCCCAAAGTGGCAACACAGTCAGGAGATGTGATAAG 296	VERSION	BC02011.1 GI:18314472
Db	379 AGCAGAGGATGTTACCAACCGTACAGATGGCAGAGATCTCATATGCAAGTG 438	KEYWORDS	MGC.
Oy	297 AACCCAAAGGATGAAATGACAGTCATAAAATGGGAGAACTCTCATATGCAAGTG 436	SOURCE	Homo sapiens.
Db	439 GATCCAGAGGACGCCAAACCGTACAGATGGCAGAGATCTCATATGCAAGTG 498	ORGANISM	Homo sapiens
Oy	357 CCCAGCTATGTCACAAAGCAATCCAAAGCTGGTGTGATGAGTACATGATTGTACTT 416	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo sapiens, (bases 1 to 1380)
Db	499 CCTACTCTGTGCTCTGCAATCCAAAGCTGACAGATCTCATATGCAAGTG 558	AUTHORS	Straubberg, R.
Oy	617 GGTGTTAGGGCCAAACTCCCACCGACTGTTGGCATTATACAGGTGTTGGTAC 476	TITLE	Direct Submission
Db	559 GGTGTTAGGGCCAAACTCCCACCGACTGTTGGTAC 618	JOURNAL	Submitted (22-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
Oy	477 TCTCATACCTGGTGGATGGAAATGCTACTGTCCTAAACAAAGTCCTAAATAC 536	REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
Db	619 TCGACTTACCAAGTAGCTGTGAATGCTGCTGGTAAATGAGTATGTCCTAAATAC 678	COMMENT	Contact: MGC help desk Email: cgaps_re@mail.nih.gov
Oy	537 TACTATGTTGCCAATATGTCCTGCTGGTAATGGCTATAAGTACTATGTCCTAT 596	Tissue	Procurement: Miklos Palkovits, M.D., Ph.D.
Db	679 TACTATGTTGCCAATATGTCCTGCTGGTAAATGAGTAAAGTGAAGATACCGTAC 738	Preparation:	CDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
Oy	597 GACAAAGGAGCCTGTGCCAGTACTGTGAGATGCTGACCAAT 656	Series:	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Db	739 GACAAAGGAGCCTGTGCCAGTACTGTGACAAAGGACTATGCAACCAAT 798	DNA Sequencing by:	Institute for Systems Biology http://www.systemsbiology.org
Oy	657 GCTTCAAGTAGCAAGTCTCATAGTAACTGTTAAAGTGTGAGCTCACATAACCTGT 716	contact:	amadan@systemsbiology.org
Db	799 ACTTGGCACTACAAAGTCTCTTAAGTACTGTGATGTTGAGAATACACTGGTGT 858	Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting	
Oy	717 AACATCAGTGTGTCAGGGACATGTGCAATGTGTCAAACGCCATTA- 775	FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Db	859 GACATGAGTACTCAAGGAAGACTGCAAGGCTACTGTGCTGTGAGAACCAATTAC 918	source	Series: IRAK Plate: 33 Row: n Column: 2
Oy	776 TAAATGGCACTACACACGGTAGGGCTATGTAGAGGGTAGCATTACTACTAG 835		This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507670.
Db	919 TCAATTACCTACTGTGAGGATGGCAAGACTGGATGGTAAGGGCTGTGATCATTAAT- 976		Location/Qualifiers
Oy	836 ATTTGGCATCTACTTACATATCTGAGAATGTAGCATTGTGATAC 895		1. .1380
Db	977 -----GCGACATACAGGGAAATGTGATGTGATGTGAC 1013		/organism="Homo sapiens"
Oy	896 ATTTGGATTCATGTTCTCTGGATGTGCTTTTACAAATATTTTC 955		/db_xref="MGC:26358 IMAGE:4826427"
Db	1014 AAATTGGATTCATGTTCTCTGGATGTGCTTTACAAATATTTTC 1073		/clone="MGC:26358 IMAGE:4826427"
Oy	956 ATACAATGGTAAACACAACTATACACACTGGATTTTATATAA 1015		/tissue_type="Testis"
Db	1074 GSCATGTTACAAAGTAGTGTGATGACACTGTGACATAAA- 1131		/clone_id="NIGM:NIH_MGC_97"
Oy	1016 CTGTGTTACATGTTCTCTGGATGTGCTTTTACAAATATTTTC 1075		/lab_host="DH10B"
Db	1132 -----TTAGTGTCTTACAGACTGAACTGAGATTTGAGATTTGAAACTTATACCA 1187		/note="vector: pBluescript"
Oy	1076 TATGACTAAGTCAAAACCCGGATGAAAGTGTGAAATATGTCCTAGACAAAT 1135		219. .950
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		BASE COUNT	448 a 289 c 280 g 363 t
		ORIGIN	
		Query Match	24.0%; Score 513.6; DB 9; Length 1380;
		Best Local Similarity	68.7%; Pred No. 8.6e-85;
		Matches	797; Conservative 0; Mismatches 324; Indels 39; Gaps 5;

Db	370	 CAACATGAACTAAGGAAGCAGTCCTCCACCTGCCAGTAACATGCTAAGATGGATGG	429	VERSION AJ001400.1	GI:2388784
Oy	237	ACAAAGAGGCTGCACCAATTGCCAAAATGGGCAACCCAGTGCAATTACAGACAG	296	CRISP-3; cysteine-rich secretory protein-3.	
Db	430	AGCAGAGGATACACRAGGATGCCAAAGGGCACAACAGTCACTTACACATAGT	489	ORGANISM Equus caballus	
Oy	297	ACCCAAAGGTCGAATGACAGTCATAAATGGTGGAGAACTCTACATGCTAAGTG	356	SOURCE	
Db	490	GATCCAGAGGACGCCAAACCGTCAAGATGGTGGAGAACTCTACATGCTAAGTG	549	ORGANISM	
Oy	357	CCAGCCTATGGTCACAAGCAATCCAAAGCTGTTGATGAGTACATGATTGACTT	416	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Db	550	CTTACTTCTGGCTCTGCTACCAAGCTGTTGACAGGATCTAGATGCTATGCTA	609	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.	
Oy	417	GGTGTAGGGCCAAGACTCCACCGAGTGGTGGACATATACAGGTTGGTGTAC	476	REFERENCE 1 (bases 1 to 1295)	
Db	610	GGTGTAGGGACCAAGAGTCCCATGCTGAGTGTGGACATTATACAGCTGTTG	669	REVISION 2 (bases 1 to 1295)	
Oy	477	TCTCATACCTGCTGGATGGAAATGCCACTAACAAAGTCTAAATAC	536	AUTHORS Schambony,A.	
Db	670	TGACTCTTACCAAGTAGGCTGTGAGATGCTCTACATGCTAAGTAAATAC	729	TITLE Direct Submission	
Oy	537	TACTATGTTGCCAATATGCTCTGGTAAATGGGCTAATAGCTATATGGCCCTT	596	JOURNAL Submitted (03-SEP-1997). Schambony A., Instiut fuer Reproduktionsmedizin, Tierärztliche Hochschule Hannover, Buenteweg 15, D-30559 Hannover, GERMANY	
Db	730	TACTATGTTGCCAATATGCTCTGGTAAATATGCTGAGTAAATGAGAATCCCGT	789	FEBS lett. 420 (2-3), 179-185 (1997)	
Oy	597	GAACAAAGGAGCACCTGTGCGGTGGCTGATGACTGTGACAAAGCTACACT	656	AUTHORS Magdaleno,L., Gasset,M., Varea,J., Schambony,A.M., Urbanke,C., Raida,M., Topfer-Petersen,E., and Calvete,J.J.	
Db	790	CAACAGGAAACCTGTGCGGTGGCTGATGACTGTGACAAAGCTACACT	849	STUDY Biochemical and conformational characterisation of Hsp-3, a stallion seminal plasma protein of the cysteine-rich secretory protein (CRISP) family	
Oy	657	GGTGCAGTACAGTCAAGATCTCTATGACTAATGTAAGTTGACCTACATAC	716	FEBS lett. 420 (2-3), 179-185 (1997)	
Db	850	AGTTGCCAGTACAGTCTCTAAGTAACTGTGATGCTGAGAATACAGCTGGT	909	PMID 9819394	
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Db	910	GAACARGAGTGTCACTCAGGAAGAAGTGCAGGCTACTGTGCTGAGAACATT	969	FEATURES	
Oy	776	TTAAATAGCCTACACCGAGTAGGCTATGAGAGGTCAGATTACTCTAGT	835	SOURCE	
Db	970	TGATTTACCTAGTGAGCATGTGCAAGACTGCATGGATAAGGGCTGCATTTA	1027	ORGANISM	
Oy	836	ATTGGCATCTACTTAGTTAACATACTAGCTGAGAAATGTTGGCAGTTGATC	895	gene	
Db	1028	-----GGCACATACCACTAGCTGAGAAATGTTGATGATGCTG 1064		/organism="Equus caballus"	
Oy	896	ACATTGATTCAATGTTCTCTGGATCTGCTTATTACAAATATTT	955	/db_xref="taxon:9796"	
Db	1065	AAATTGATTCAACAGCAATGCTCTCCCGATCATCACAGAAATCTATCA	1124	/sex="Male"	
Oy	956	ATACAAATGTTAAAGAACAACTTACACAACTTGGATTATATATAAA	1015	/tissue-type="ampulla"	
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Db	1183	---TTAGCTTAAACGACTGATGAGTGGATTGAACTGTATACCA	1238	/gene="crisp-3"	
Oy	1076	TATGACTAATCTACTAAACCTGGATGAAAGTAAATTGTCCTGAGAACAA	1135	/codon_start=1	
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Oy	1136	GTACAAAGAACAAATAA	1155	/protein_id="CAA04729.1"	
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				Db 24 TAACAGCATGCCTCACCTTGCTGCTGAGAACCA--ACATGCATATTACAGTGCTG	
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				Db 81 TGTTCCTGCTGGCTCCATTTTCAGCAATGAGATAGGATCCCTT	
				137	
				Query 124 TRACTGCTTGTGAACTACACCAACACAGTCACAGGAGATGTCAGATGACATG	
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				Db 138 TGTCTGTTGTGCAATGCCAACAGCAAGTCCAAAGAGATGTCAGATGACATG	
				197	
				Query 184 AACTGAGGAGCAGTCTCCCTGCCAGAACATGTCAGATGGAAGCAAG	
				243	
				Db 198 ACTTAAGGAGACAGTCCTCCACTTCCAGTACATGCAATGTCAGTGGACAGCA	
				257	
				Query 244 AGGCTGCCAAATGCCAACAGTGGCCAAACAGTCACATGCAAGTACCCAA	
				303	
				Db 258 AGACAGCAAAATGCCAACAGTGGCCAAACAGTCACATGCAAGTAAAGCAG	
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				Query 304 AGGATCG--AATGACAGTCATAAATGTTGAGATCTCATGTCAGTGC	
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Db	318 AAGATCGCGCAGTCGGTACATGAAATGTTGAGATCTCTTATGTCAGTATACCA	377		REFERENCE	96354287
Qy	361 GCTCATGGTACACAACTTCAACGGTTGATGACTACAGTATTGACTTGGG	420		PUBMED	915720
Db	378 ATTCCTGGTCAGATGCAATCAAATGGCATGATGAGGGCCAGATTAAATAGGG	437		AUTHORS	2 (bases 1 to 1388)
Qy	421 TAGGCCAARAAGACTCCAAAGGCCAGTGGTGAATTACACAGGTTGTTGACTCT	480		TITLE	Foster, J.A. and Gerton, G.L.
Db	438 TGGGCCAARAAGACTCCAAAGGCCAGTGGTGAATTACACAGGTTGTTGACTCT	497		JOURNAL	Direct Submission
Qy	481 CATTACCTGTTGATGTTGAAATGCTACTGTCCTAACATCAAATGGCATGATGAGG	540		Submitted (08-SEP-1995) James A. Foster, Department of Obstetrics and Gynecology, Division of Reproductive Biology, University of Pennsylvania, 36th and Hamilton Walk, Philadelphia, PA 19104, USA	
Db	498 CTTACCGTGTGATGTTGAAATGCTATGTCCTAACACAGGTTGTTGACTCT	557		LOCATION	Location/Qualifiers
Qy	541 ATGTTGGCAATATGTCCTGTTAATGGCTATAGCTATAGCTATGTCCTTGTGAC	600		1..1388	
Db	558 ATGTTGGCAATATGTCCTGCTGTTGAAATGCTAACATCAAATGGCATGATGAC	617		ORGANISM	"Cavia porcellus"
Qy	601 AAGGAGCACCTTGTGCCGTTGCCGTTGCTGACTGACGATGACTGACATGGT	660		STRAIN	"Hartley"
Db	618 AAGGACACCTTGTGCCGTTGCCGTTGCTGACTGACGATGACTGACATGGT	677		DB_XREF	"GI:1016156"
Qy	661 GCAACTAGAGATCTATAGTAAAGTTGAGCTGACGATGACTGACATGGT	720		TRANSLATION	"MALLVVVFLTMILPCVLTJNGKPAFTALITLITOSOVONEIINKHQLRKSVPASSMLKMRNSREAVNQWNLKHNPDKRSTKCGNLMSDPRSSWSDAQSWSWDESDPTFGVGPKSIHNVGHYDOLWVSYLVCVGIACPNQO
Db	678 GCGAGTATGAGATCCTGTTAGTACTGTGATTCCTGTAAGAAATAGCTGGCTGAA	737		KNTAGRCOLVERKKAACRCEDKI"	
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Db	738 ATGAAATGTCGAAGAAACTGCAAGTACACTTGTCAATGTAACAAATTACTGAA	797			
Qy	781 TACGGATTACACCGAGTAGGCTATGAGGAGGAGTCAGATTACTAGATTG	840			
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Qy	901 TGTTCATAATGTTCTCTGTTCTGTTTATTACAAATATTTCTACAA	960			
Db	894 TGATTCACAA-CCGTAATGTCATCTCTGTTCTACAGAACATCTTCACACA	951			
Qy	961 AATGGTTAAAGAACAAATCTAACACAACTTGGATTATATTAACCTG	1020			
Db	952 ATGATTCACAAAGCAGTAGTCTGTGATGACACTTGGCT--GATATAATTG	1008			
Qy	1021 TGTATTAATTACTGAAATTATGGGTGAAMATTGAGTTGTTATTCATGAA	1080			
Db	1009 TACTTTAAATGTTAAATGATCA-ATGGAGATTGTAAGTTGATAACCTAAGA	1067			
Qy	1081 CTAACTTCACTAAACCTGTTGAAAGTAAATTGTTCTCTAGAACAAATGTAC	1139			
Db	1068 CTTAGTCCCTAGAACTTGGATTAAACGAAATTACATGTTCTGAACACATGC	1126			
RESULT 1					
CPP35712	1388 bp mRNA linear ROD 18-JUN-1996				
LOCUS	Cavia porcellus acrosomal autoantigen 1 mRNA, complete cds.				
DEFINITION					
ACCESSION	U35712				
VERSION	U35712.1				
KEYWORDS	1 (bases 1 to 1388)				
SOURCE	Foster, J.A. and Gerton, G.L.				
ORGANISM	Cavia porcellus.				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.					
REFERENCE					
AUTHORS					
TITLE	Autoantigen 1 of the guinea pig sperm acrosome is the homologue of mouse Tax-1 and human TPX1 and is a member of the cysteine-rich secretory protein (CRISP) family				
JOURNAL	Mol. Reprod. Dev. 44 (2), 221-229 (1996)				
Qy	294 AGTAACCAAAGGATGCAAGTCAATGTCATAATGTTGAGAATCTCATGTCAGT	353			
Db	434 AGTATCCAGACGTCAGTCAAAACNGCAGCAAAATGTTGAGAATCTCATGTCAGT	493			
Qy	354 GCCCCAGCTCATGTCAGTCAAAACNGCAGCAAAATGTTGAGAATCTCATGTCAGT	413			
Db	494 GACCCTAGTCCTGGTCAGATGCAATCCAAAGCTGTTGATGAGGACATGCTTAC	553			
Qy	414 TTGSGTGGGCCAAGCTCCACGCGTGGGCAATTACAGCTGTTGTTG	473			
Db	554 TTGGAGTGGACCAAGGACTCACATGCGTTGAGCATCACAGCTGTTG	613			
Qy	474 TACTCTCATCTGGTGAATTGCTACTGCCCACATCAAAGTCTAA	533			
Db	614 TATCGTCTTATCTGTTGCTGTTGAATGCTACTGCCCACATCAAAGCTAA	673			
Qy	534 TACTACTATGTTGCCAAATATGTCCTGCTGTTAATGGCCTAATAGACTATATGTCCT	593			

QY 936 ATTTCACAAATTTCTACAAATGGTTAAAAGAACAACTACACACAC 995
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RESULT 13

AB009662 AB009662 1280 bp mRNA linear ROD 01-AUG-1998
 LOCUS Rattus norvegicus mRNA for testis specific protein, complete Cds.
 DEFINITION AB009662
 ACCESSION AB009662
 VERSION 1 GI:3374579
 KEYWORDS testis specific protein.
 SOURCE Rattus norvegicus (strain:ponryu) 20 days after birth male Testis
 ORGANISM Spermatogenic cells cDNA to mRNA, clone:tpx-1.
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 1280)
 AUTHORS Meda,T., Sakashita,M., Oba,Y. and Nakaniishi,Y.
 TITLE Molecular cloning of the rat Tpx-1 responsible for the interaction
 between spermatogenic and Sertoli cells
 JOURNAL Biochem. Biophys. Res. Commun. 248 (1), 140-146 (1998)
 MEDLINE 93340664
 REFERENCE 2 (bases 1 to 1280)
 AUTHORS Nakaniishi,Y.
 TITLE Direct Submission
 JOURNAL Submitted (11-DEC-1997) Yoshinobu Nakaniishi, Kanazawa University,
 Faculty of Pharmaceutical Sciences; 13-1 Takara-machi, Kanazawa,
 Ishikawa 920, Japan (Tel:076-234-4480, Fax:076-234-4480)
 FEATURES source

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 ORIGIN

Qy 17.2% Score 367.8; DB 10; Length 1280;
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 Db 130 CACCCACAGGAAGGATCCAGCTCGCTACTTGACACCAACACATACAGTC 189
 Qy 157 AAAGSGAGATGTGAATAGCACAATGACTGAGGAGAGTACTCCCTGCAGA 216
 Db 190 AAAGAGAGATCATAGCTAACACATGACTGAGGAGACAGTTAGCCCTGCGACA 249
 Qy 217 ACATGCTGAGATGGATGGACAAAGGGCTGACCAATGCCAAGTGGCAAC 276
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 Db 370 ATCTCTATCTGACTGACCTATCTGGAGACCT 429
 Qy 397 AGTACATGATGTTGACTTGTGTTAGGAGCTTACCTTAACTGAGCT 456
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DEFINITION	AF078552 AF078552 Rattus norvegicus cysteine-rich secretory protein-2 CRISP-2 (tpx-1) mRNA, complete cds.	Db	476 ACTGCAATTAGAACACAGCTAACCCAAAGGTGCAAGTCAGCTCAAATGCTGGAGA 535
ACCESSION	AF078552 AF078552	QY	337 ATCTCTACATGTCAGTGCCGCCAGCTATGTCAGTCAGAACGCAATCCAAAGCAGCTGGTTGATG 396
VERSION	1432 bp	Db	536 ATCTCTATGTCAGTGACGACCTACATCTCTGAGAACGGTAAATCAGCTGGATGAG 595
KEYWORDS	linear ROD 11-AUG-1999	QY	397 ACTACATGATTTGACTTGTGTAGGCCAACGSCAGTGTGGACATT 456
SOURCE	ORGANISM Rattus norvegicus.	Db	596 AAAATGAAACCTCGTTCTCGCGTAGGCTAA---ACCCAAATCGCTGCGGACAT 652
JOURNAL	Rattus norvegicus.	QY	457 ATACACAGGTTCTTGTACTCTCTCATCTCTGTTGATGAGGAATGCCACTGTCCA 516
MEDLINE	1 (bases 1 to 1432)	Db	653 ACACTCAGCTGTTGTTGATCTCATCTCTCAAGTGGATGPGAGSTGCTFACTGFOCA 712
REFERENCE	O'Bryan, M.K., Loveland, K.L., Herszfeld, D., McFarlane, J.R., Hearn, M.T. and de Kretser, D.M.	QY	517 ATCAAAGTCTAAATCTACTACTATGTTGCCAATATGTCCTGCTGTAAATGGCTA 576
AUTHORS	Identification of a rat testis-specific gene encoding a potential rat outer dense fibre protein	Db	713 ATCAAGATACCTGTAATCTCTATGTTGCCATTTACTGCTTGTCAAACAGTGA 772
TITLE	Direct Submission	QY	577 ATAGACTATATGCTCCCTATGACAAAGGACCTGTGCGAGTGCCAGATAACTGTG 636
JOURNAL	Submitted (15-JUL-1998) Institute of Reproduction & Development, Monash University, Monash Medical Centre, 246 Clayton Rd., Clayton, Victoria 3168, Australia	Db	773 TGAAGAAAGTAGACCCCATATCATCATACTGAGAACACTTGTGCTAGTGTCCATAACTGTG 832
FEATURES	Location/Qualifiers	QY	637 AGATGGACTATGACCAATGGTCAGTAGGAACTCTCTATAGTTGCTCAAATGTT 696
source	I.. 1432	Db	833 ATAATGCTTGTGACCAAATGCTGTTGAGAATCTACTCTATAGTACTCTAAAGTT 892
gene	/organism="Rattus norvegicus" 'strain'='Sprague-Dawley' 'Ab.xref'='taxon:10116'	QY	697 TGAGCTCATACTAACCTGAAATCATGAGTGTGAGAATCTACTGCTCAAATGCA 756
CDS	I.. 1432	Db	893 TGAGAGTCTGACGACGGTGTAACTGAGTGTCTCANGCAAGTGTGAGCTACTGCC 952
gene	/gene="tpx-1"	QY	757 ATGGTCAACACGATTATAAATAGCATTACACCCGAGTAGGGCTATGAGAG 815
fibers	/note="putative component of sperm tail outer dense	Db	953 TATGTGAGGACAAATTCATACATGCCAGCGTGCAGCATGAGGG 1012
codon_start	I.. 1432	QY	816 GACTCAGATTACTACTAGTTGGACTACTTAGTTACATATAGTTACATATAGCTGAGAA 875
product	/product="cysteine-rich secretory protein-2 CRISP-2"	Db	1013 GGGTACAGACTTAGTGTGAGCTT 1046
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BASE COUNT	458 a 301 c 299 g 373 t	QY	1056 TTGAAAGTTGATCTCATGACTAGTGTCACTAACCTGGATGA 1107
ORIGIN	1 others	Db	1222 TTGGAAGTTGACCATGACTGTGTCATCTGACTAACCTGGATGA 1273
Query Match	16.9%; Score 362.2; DB 10; Length 1432;	RESULT	15
Best Local Similarity	63.0%; Pred. No. 6.2e-57; Matches 675; Conservative 0; Mismatches 359; Indels 38; Gaps 6;	REF	1 (bases 1 to 1498)
QY	37 CTGCAATGACATATTCCAGTGCTGTCCTGGTGTGGCTCTTCATCTTC 96	RATREG	RATREG
Db	239 CAGCCATGGCTGGTCAGGATGCGTGTCTCTGCTTCTACCA--TGTC 295	LOCUS	RATREG
QY	97 CAGCAATGACATTAAGATCCGGTTACCTGCTTACACCAACACAGTC 156	DEFINITION	Rat epididymal glycoprotein (AEG) mRNA, complete cds.
Db	296 CAGCCATGGACGAAAGATCCAGCTTGCTACTTGACACCAACAACTTC 355	VERSION	M3117.1 GI:202772
QY	157 AAGGGAGATTGTAATGACCAATGACTAGGAGAGCAGTACATGAGCA 216	KEYWORDS	epididymal glycoprotein.
Db	356 AAGAGAGTCATGCTTACACATGACTAGGAGAGCAGTACATGAGCA 415	SOURCE	Rattus norvegicus (strain Sprague-Dawley) adult epididymus cDNA to mRNA.
QY	217 AATGCTGAGTGGAGTGGAGAACAAAGGGCTGAGCAATGGCAACC 276	ORGANISM	Rattus norvegicus
REFERENCE	1 (bases 1 to 1498)		

